Chirag J Patel

List of Publications by Year
in descending order

123 papers	5,170 citations	101384 36 h-index	102304 66 g-index
146 all docs	146 docs citations	146 times ranked	9266 citing authors

#	Article	IF	Citations
1	An Environment-Wide Association Study (EWAS) on Type 2 Diabetes Mellitus. PLoS ONE, 2010, 5, e10746.	1.1	470
2	Ethnic Differences in the Relationship Between Insulin Sensitivity and Insulin Response. Diabetes Care, 2013, 36, 1789-1796.	4.3	449
3	Unprocessed Red Meat and Processed Meat Consumption: Dietary Guideline Recommendations From the Nutritional Recommendations (NutriRECS) Consortium. Annals of Internal Medicine, 2019, 171, 756.	2.0	227
4	A standard database for drug repositioning. Scientific Data, 2017, 4, 170029.	2.4	224
5	The Landscape of Genetic Content in the Gut and Oral Human Microbiome. Cell Host and Microbe, 2019, 26, 283-295.e8.	5.1	207
6	Assessment of vibration of effects due to model specification can demonstrate the instability of observational associations. Journal of Clinical Epidemiology, 2015, 68, 1046-1058.	2.4	183
7	Current Challenges and New Opportunities for Gene-Environment Interaction Studies of Complex Diseases. American Journal of Epidemiology, 2017, 186, 753-761.	1.6	150
8	Mendelian randomization study of adiposity-related traits and risk of breast, ovarian, prostate, lung and colorectal cancer. International Journal of Epidemiology, 2016, 45, 896-908.	0.9	124
9	Systematic evaluation of environmental factors: persistent pollutants and nutrients correlated with serum lipid levels. International Journal of Epidemiology, 2012, 41, 828-843.	0.9	123
10	A Nutrient-Wide Association Study on Blood Pressure. Circulation, 2012, 126, 2456-2464.	1.6	122
11	Systematic evaluation of environmental and behavioural factors associated with all-cause mortality in the United States National Health and Nutrition Examination Survey. International Journal of Epidemiology, 2013, 42, 1795-1810.	0.9	109
12	Systematic identification of interaction effects between genome- and environment-wide associations in type 2 diabetes mellitus. Human Genetics, 2013, 132, 495-508.	1.8	98
13	Informatics and Data Analytics to Support Exposome-Based Discovery for Public Health. Annual Review of Public Health, 2017, 38, 279-294.	7.6	97
14	Placing epidemiological results in the context of multiplicity and typical correlations of exposures. Journal of Epidemiology and Community Health, 2014, 68, 1096-1100.	2.0	94
15	Studying the Elusive Environment in Large Scale. JAMA - Journal of the American Medical Association, 2014, 311, 2173.	3.8	94
16	Evolving phenotypes of non-hospitalized patients that indicate long COVID. BMC Medicine, 2021, 19, 249.	2.3	87
17	A database of human exposomes and phenomes from the US National Health and Nutrition Examination Survey. Scientific Data, 2016, 3, 160096.	2.4	85
18	Update on the State of the Science for Analytical Methods for Gene-Environment Interactions. American Journal of Epidemiology, 2017, 186, 762-770.	1.6	79

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19	Urinary Triclosan is Associated with Elevated Body Mass Index in NHANES. PLoS ONE, 2013, 8, e80057.	1.1	78
20	In the Era of Precision Medicine and Big Data, Who Is Normal?. JAMA - Journal of the American Medical Association, 2018, 319, 1981.	3.8	76
21	Analysis of the Genetic Basis of Disease in the Context of Worldwide Human Relationships and Migration. PLoS Genetics, 2013, 9, e1003447.	1.5	67
22	Disease Risk Factors Identified Through Shared Genetic Architecture and Electronic Medical Records. Science Translational Medicine, 2014, 6, 234ra57.	5.8	58
23	The Exposome Research Paradigm: an Opportunity to Understand the Environmental Basis for Human Health and Disease. Current Environmental Health Reports, 2017, 4, 89-98.	3.2	58
24	MeSHDD: Literature-based drug-drug similarity for drug repositioning. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 614-618.	2.2	58
25	Systematic correlation of environmental exposure and physiological and self-reported behaviour factors with leukocyte telomere length. International Journal of Epidemiology, 2017, 46, dyw043.	0.9	54
26	Diabetes Severity, Metabolic Syndrome, and the Risk of Erectile Dysfunction. Journal of Sexual Medicine, 2013, 10, 3102-3109.	0.3	52
27	Repurposing large health insurance claims data to estimate genetic and environmental contributions in 560 phenotypes. Nature Genetics, 2019, 51, 327-334.	9.4	52
28	Perspective: Improving Nutritional Guidelines for Sustainable Health Policies: Current Status and Perspectives. Advances in Nutrition, 2017, 8, 532-545.	2.9	51
29	Analytic Complexity and Challenges in Identifying Mixtures of Exposures Associated with Phenotypes in the Exposome Era. Current Epidemiology Reports, 2017, 4, 22-30.	1.1	49
30	Exposome-wide association study of semen quality: Systematic discovery of endocrine disrupting chemical biomarkers in fertility require large sample sizes. Environment International, 2019, 125, 505-514.	4.8	48
31	Whole genome sequencing in support of wellness and health maintenance. Genome Medicine, 2013, 5, 58.	3.6	46
32	ksRepo: a generalized platform for computational drug repositioning. BMC Bioinformatics, 2016, 17, 78.	1.2	46
33	A review of validation strategies for computational drug repositioning. Briefings in Bioinformatics, 2018, 19, 174-177.	3.2	46
34	Conducting a Reproducible Mendelian Randomization Analysis Using the R Analytic Statistical Environment. Current Protocols in Human Genetics, 2019, 101, e82.	3.5	45
35	Natural Language Processing–Enabled and Conventional Data Capture Methods for Input to Electronic Health Records: A Comparative Usability Study. JMIR Medical Informatics, 2016, 4, e35.	1.3	43
36	Investigation of maternal environmental exposures in association with self-reported preterm birth. Reproductive Toxicology, 2014, 45, 1-7.	1.3	42

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37	Investigation of Dietary Factors and Endometrial Cancer Risk Using a Nutrient-wide Association Study Approach in the EPIC and Nurses' Health Study (NHS) and NHSII. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 466-471.	1.1	42
38	Toward Capturing the Exposome: Exposure Biomarker Variability and Coexposure Patterns in the Shared Environment. Environmental Science & Technology, 2018, 52, 8801-8810.	4.6	40
39	Comparative analyses of population-scale phenomic data in electronic medical records reveal race-specific disease networks. Bioinformatics, 2016, 32, i101-i110.	1.8	39
40	Environment-Wide Association Study of Blood Pressure in the National Health and Nutrition Examination Survey (1999â€"2012). Scientific Reports, 2016, 6, 30373.	1.6	38
41	Systematic Assessment of the Correlations of Household Income With Infectious, Biochemical, Physiological, and Environmental Factors in the United States, 1999â€"2006. American Journal of Epidemiology, 2015, 181, 171-179.	1.6	36
42	Trypsin-encoding <i>PRSS1-PRSS2</i> variations influence the risk of asparaginase-associated pancreatitis in children with acute lymphoblastic leukemia: a Ponte di Legno toxicity working group report. Haematologica, 2019, 104, 556-563.	1.7	36
43	Comparisons of Polyexposure, Polygenic, and Clinical Risk Scores in Risk Prediction of Type 2 Diabetes. Diabetes Care, 2021, 44, 935-943.	4.3	35
44	DEVELOPMENT OF EXPOSOME CORRELATION GLOBES TO MAP OUT ENVIRONMENT-WIDE ASSOCIATIONS. , 2014, , .		34
45	Characteristics of undiagnosed diabetes in men and women under the age of 50 years in the Indian subcontinent: the National Family Health Survey (NFHS-4)/Demographic Health Survey 2015â€"2016. BMJ Open Diabetes Research and Care, 2020, 8, e000965.	1.2	34
46	Gene-level metagenomic architectures across diseases yield high-resolution microbiome diagnostic indicators. Nature Communications, 2021, 12, 2907.	5.8	33
47	Field-wide meta-analyses of observational associations can map selective availability of risk factors and the impact of model specifications. Journal of Clinical Epidemiology, 2016, 71, 58-67.	2.4	31
48	EGFR-targeted intraoperative fluorescence imaging detects high-grade glioma with panitumumab-IRDye800 in a phase 1 clinical trial. Theranostics, 2021, 11, 7130-7143.	4.6	31
49	Development of exposome correlation globes to map out environment-wide associations. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 231-42.	0.7	31
50	Cancer Cluster Investigations: Review of the Past and Proposals for the Future. International Journal of Environmental Research and Public Health, 2014, 11, 1479-1499.	1.2	30
51	Nutrient-wide association study of 57 foods/nutrients and epithelial ovarian cancer in the European Prospective Investigation into Cancer and Nutrition study and the Netherlands Cohort Study. American Journal of Clinical Nutrition, 2016, 103, 161-167.	2.2	29
52	Data-driven integration of epidemiological and toxicological data to select candidate interacting genes and environmental factors in association with disease. Bioinformatics, 2012, 28, i121-i126.	1.8	28
53	Systematic assessment of pharmaceutical prescriptions in association with cancer risk: a method to conduct a population-wide medication-wide longitudinal study. Scientific Reports, 2016, 6, 31308.	1.6	28
54	Covariate selection for association screening in multiphenotype genetic studies. Nature Genetics, 2017, 49, 1789-1795.	9.4	27

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55	Opportunities and Challenges for Environmental Exposure Assessment in Population-Based Studies. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1370-1380.	1.1	27
56	A multi-omic analysis of birthweight in newborn cord blood reveals new underlying mechanisms related to cholesterol metabolism. Metabolism: Clinical and Experimental, 2020, 110, 154292.	1.5	25
57	Predicting environmental chemical factors associated with disease-related gene expression data. BMC Medical Genomics, 2010, 3, 17.	0.7	24
58	A systematic machine learning and data type comparison yields metagenomic predictors of infant age, sex, breastfeeding, antibiotic usage, country of origin, and delivery type. PLoS Computational Biology, 2020, 16, e1007895.	1.5	21
59	Utilizing a Biology-Driven Approach to Map the Exposome in Health and Disease: An Essential Investment to Drive the Next Generation of Environmental Discovery. Environmental Health Perspectives, 2021, 129, 85001.	2.8	20
60	Analytical Complexity in Detection of Gene Variant-by-Environment Exposure Interactions in High-Throughput Genomic and Exposomic Research. Current Environmental Health Reports, 2016, 3, 64-72.	3.2	18
61	Examining the robustness of observational associations to model, measurement and sampling uncertainty with the vibration of effects framework. International Journal of Epidemiology, 2021, 50, 266-278.	0.9	18
62	Systematic identification of correlates of HIV infection. Aids, 2018, 32, 933-943.	1.0	17
63	Using deep learning to predict abdominal age from liver and pancreas magnetic resonance images. Nature Communications, 2022, 13, 1979.	5.8	17
64	Prediction of chronological and biological age from laboratory data. Aging, 2020, 12, 7626-7638.	1.4	16
65	Integrated Analysis of Gene Expression Differences in Twins Discordant for Disease and Binary Phenotypes. Scientific Reports, 2018, 8, 17.	1.6	15
66	Scalability and cost-effectiveness analysis of whole genome-wide association studies on Google Cloud Platform and Amazon Web Services. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 1425-1430.	2.2	15
67	Computational repositioning and preclinical validation of mifepristone for human vestibular schwannoma. Scientific Reports, 2018, 8, 5437.	1.6	14
68	Model-Averaged Confounder Adjustment for Estimating Multivariate Exposure Effects with Linear Regression. Biometrics, 2018, 74, 1034-1044.	0.8	13
69	Signals Among Signals: Prioritizing Nongenetic Associations in Massive Data Sets. American Journal of Epidemiology, 2019, 188, 846-850.	1.6	13
70	Age-dependent co-dependency structure of biomarkers in the general population of the United States. Aging, 2019, 11, 1404-1426.	1.4	13
71	Systematically assessing microbiome–disease associations identifies drivers of inconsistency in metagenomic research. PLoS Biology, 2022, 20, e3001556.	2.6	13
72	Leveraging vibration of effects analysis for robust discovery in observational biomedical data science. PLoS Biology, 2021, 19, e3001398.	2.6	12

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73	A nutrient-wide association study for risk of prostate cancer in the European Prospective Investigation into Cancer and Nutrition and the Netherlands Cohort Study. European Journal of Nutrition, 2020, 59, 2929-2937.	1.8	11
74	Characterising the relationships between physiological indicators and all-cause mortality (NHANES): a population-based cohort study. The Lancet Healthy Longevity, 2021, 2, e651-e662.	2.0	11
75	Metabolites, Nutrients, and Lifestyle Factors in Relation to Coffee Consumption: An Environment-Wide Association Study. Nutrients, 2020, 12, 1470.	1.7	11
76	Temporal exposure and consistency of endocrine disrupting chemicals in a longitudinal study of individuals with impaired fasting glucose. Environmental Research, 2021, 197, 110901.	3.7	10
77	Family History–Wide Association Study to Identify Clinical and Environmental Risk Factors for Common Chronic Diseases. American Journal of Epidemiology, 2019, 188, 1563-1568.	1.6	8
78	Diverse experts' perspectives on ethical issues of using machine learning to predict HIV/AIDS risk in sub-Saharan Africa: a modified Delphi study. BMJ Open, 2021, 11, e052287.	0.8	8
79	Use of Flexible Endoscopic Scissors to Cut Obstructing Suture Material in Gastric Bypass Patients. Obesity Surgery, 2008, 18, 336-339.	1.1	7
80	Aether: leveraging linear programming for optimal cloud computing in genomics. Bioinformatics, 2018, 34, 1565-1567.	1.8	7
81	Systematic detection of positive selection in the human-pathogen interactome and lasting effects on infectious disease susceptibility. PLoS ONE, 2018, 13, e0196676.	1.1	7
82	Informatics can help providers incorporate context into care. JAMIA Open, 2018, 1, 3-6.	1.0	6
83	Laboratory€wide association study of survival with prostate cancer. Cancer, 2021, 127, 1102-1113.	2.0	6
84	METHODS TO ENHANCE THE REPRODUCIBILITY OF PRECISION MEDICINE. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 180-182.	0.7	6
85	Development and validation pathways of artificial intelligence tools evaluated in randomised clinical trials. BMJ Health and Care Informatics, 2021, 28, e100466.	1.4	6
86	Identification of occupations susceptible to high exposure and risk associated with multiple toxicants in an observational study: National Health and Nutrition Examination Survey 1999–2014. Exposome, 2022, 2, .	1.2	6
87	Perspective: Beyond the genome. Nature, 2016, 537, S105-S105.	13.7	5
88	Plasma metabolomics of autism spectrum disorder and influence of shared components in proband families. Exposome, 2021, 1, osab004.	1.2	5
89	Integrated molecular response of exposure to traffic-related pollutants in the US trucking industry. Environment International, 2022, 158, 106957.	4.8	5
90	Shared exposure liability of type 2 diabetes and other chronic conditions in the UK Biobank. Acta Diabetologica, 2022, 59, 851-860.	1.2	5

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91	Exposome-wide ranking of modifiable risk factors for cardiometabolic disease traits. Scientific Reports, 2022, 12, 4088.	1.6	5
92	Rcupcake: an R package for querying and analyzing biomedical data through the BD2K PIC-SURE RESTful API. Bioinformatics, 2018, 34, 1431-1432.	1.8	4
93	Secular Trends in Prevalence of Heart Failure Diagnosis over 20 Years (from the US NHANES). American Journal of Cardiology, 2022, , .	0.7	4
94	Comment: Addressing the Need for Portability in Big Data Model Building and Calibration. Journal of the American Statistical Association, 2016, 111, 127-129.	1.8	3
95	Introduction to Environment and Exposome-Wide Association Studies: A Data-Driven Method to Identify Multiple Environmental Factors Associated with Phenotypes in Human Populations. , 2018, , 129-149.		3
96	Leveraging Population-Based Clinical Quantitative Phenotyping for Drug Repositioning. CPT: Pharmacometrics and Systems Pharmacology, 2018, 7, 124-129.	1.3	3
97	Using Big Data to Determine Reference Values for Laboratory Tests—Reply. JAMA - Journal of the American Medical Association, 2018, 320, 1496.	3.8	3
98	Data-driven assessment, contextualisation and implementation of 134 variables in the risk for type 2 diabetes: an analysis of Lifelines, a prospective cohort study in the Netherlands. Diabetologia, 2021, 64, 1268-1278.	2.9	3
99	Clinical laboratory tests associated with survival in patients with metastatic renal cell carcinoma: A Laboratory Wide Association Study (LWAS). Urologic Oncology: Seminars and Original Investigations, 2022, 40, 12.e23-12.e30.	0.8	3
100	Association of 152 Biomarker Reference Intervals with All-Cause Mortality in Participants of a General United States Survey from 1999 to 2010. Clinical Chemistry, 2021, 67, 500-507.	1.5	3
101	Prevalence of Fatty Liver Disease is Driven by Prediabetes and Diabetes: US NHANES 2017–2018. Clinical Gastroenterology and Hepatology, 2022, 20, 712-713.	2.4	2
102	METHODS TO ENHANCE THE REPRODUCIBILITY OF PRECISION MEDICINE. , 2016, , .		2
103	Using Cartesian Doubt To Build a Sequencing-Based View of Microbiology. MSystems, 2021, 6, e0057421.	1.7	2
104	Genetic Variability in Molecular Responses to Chemical Exposure. Exs, 2012, 101, 437-457.	1.4	2
105	REPRODUCIBLE AND SHAREABLE QUANTIFICATIONS OF PATHOGENICITY. , 2016, , .		2
106	Exposome-Wide Association Studies: A Data-Driven Approach for Searching for Exposures Associated with Phenotype. , 2019, , 315-336.		2
107	Systematic identification of interaction effects between validated genome- and environment-wide associations on Type 2 Diabetes Mellitus. AMIA Summits on Translational Science Proceedings, 2013, 2013, 135.	0.4	2
108	The Exposome: An Approach Toward a Comprehensive Study of Exposures in Disease. , 2019, , 770-779.		1

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109	A unique presentation, and management, of acute urinary retention in a young boy with underlying vesicoureteral reflux. Journal of Surgical Case Reports, 2013, 2013, rjt047-rjt047.	0.2	0
110	aRrayLasso: a network-based approach to microarray interconversion: Fig. 1.. Bioinformatics, 2015, 31, btv469.	1.8	0
111	CBMT-08. COMPARISON OF THREE METABOLIC PET RADIOTRACERS IN GLIOBLASTOMA: CELL CULTURE AND ANIMAL STUDIES. Neuro-Oncology, 2018, 20, vi34-vi34.	0.6	0
112	CBMT-03. A NOVEL METABOLIC PET TRACER STRATEGY TO DETERMINE EARLY EFFECTS OF TUMOR TREATING FIELDS (TTFIELDS). Neuro-Oncology, 2018, 20, vi32-vi33.	0.6	0
113	CBMT-07. EVALUATION OF GLYCOLYTIC RESPONSE TO SEVEN CLASSES OF ANTI-GLIOBLASTOMA DRUGS BY NON-INVASIVE MEASUREMENT OF PYRUVATE KINASE M2. Neuro-Oncology, 2018, 20, vi33-vi34.	0.6	0
114	BIMG-16. TRACKING TTFIELDS-INDUCED ALTERATIONS IN GLIOBLASTOMA METABOLISM WITH [18F]DASA-23, A NON-INVASIVE PROBE OF PYRUVATE KINASE M2 (PKM2). Neuro-Oncology Advances, 2021, 3, i4-i4.	0.4	0
115	Common Genetic Variants in Trypsin Regulating Genes Are Associated with AsparAginase-Associated Pancreatitis in Children with Acute Lymphoblastic Leukemia: A Ponte Di Legno Toxicity Working Group Study. Blood, 2017, 130, 885-885.	0.6	0
116	What about the environment? Leveraging multi-omic datasets to characterize the environment's role in human health. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2021, 26, 309-315.	0.7	0
117	What about the environment? Leveraging multi-omic datasets to characterize the environmentâ€™s role in human health. , 2020, , .		0
118	Title is missing!. , 2020, 16, e1007895.		0
119	Title is missing!. , 2020, 16, e1007895.		0
120	Title is missing!. , 2020, 16, e1007895.		0
121	Title is missing!. , 2020, 16, e1007895.		0
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123	Title is missing!. , 2020, 16, e1007895.		0